

## CLAIMS

1. A method for inhibiting the proliferation of a pathogen or a cell infected with an pathogen, wherein the pathogen expresses an iECTA enzyme, comprising contacting the pathogen or the cell with an effective amount of an iECTA prodrug that is activated to a toxin by the pathogen or in the cell by the iECTA enzyme, thereby inhibiting the proliferation of the pathogen or the cell.
2. The method of claim 1, wherein the iECTA enzyme is selected from the group of enzymes listed in Figures 7A and B and their biological equivalents.
3. The method of claim 2, wherein the iECTA enzymes beta-lactamase and peptide deformylase are specifically excluded.
4. The method of claim 1, wherein the iECTA enzyme is a member selected from the group consisting of the enzymes designated EC1, EC2, EC3, EC4, EC5, and EC6.
5. The method of claim 1, wherein the pathogen is selected from the group consisting of bacteria, parasites, rickettsia, virus, and fungus.
6. The method of claim 1, wherein the contacting is *in vitro* or *in vivo*.
7. A method for screening for a therapeutic agent that selectively inhibits the growth of pathogen or a pathogen-infected cell, comprising contacting the pathogen or the cell with an effective amount of an iECTA prodrug that is activated to a toxin by the pathogen or in the cell by the iECTA enzyme and assaying for inhibition growth of the pathogen or the cell.
8. The method of claim 7, wherein the iECTA enzyme is selected from the group of enzymes listed in Figures 7A and 7B, and their biological equivalents.

9. The method of claim 7, wherein the enzyme is a member of an enzyme selected from the group consisting of the enzymes designated EC1, EC2, EC3, EC4, EC5, and EC6.
10. The method of claim 7, wherein the iECTA enzymes beta-lactamase and peptide deformylase are specifically excluded.
11. The method of claim 7, wherein the enzyme is a member of the group consisting of the enzymes designated EC1, EC2, EC3, EC4, EC5, and EC6.
12. The method of claim 7, wherein the pathogen is selected from the group consisting of bacteria, parasites, rickettsia, virus, and fungus.
13. The method of claim 7, wherein the contacting is *in vitro* or *in vivo*.
14. The method of claim 7, further comprising delivering to a normal, non-infected counterpart cell to the infected host cell, an effective amount of the iECTA prodrug and assaying the normal, non-infected cell for inhibition of cell growth or cytotoxicity.
15. The method of claim 7, wherein the host cell is infected with a pathogen that expresses or induces the expression of an enzyme that is selectively expressed by the pathogen.
16. The method of claim 14, wherein the normal, non-infected counterpart is a plant cell or an animal cell.
17. The method of claim 16, wherein the animal cell is a mammalian cell.
18. A method for identifying drug targets, comprising:
  - a. searching a first data structure to obtain a first set of information, wherein the first set of information comprises first enzymes associated with a target organism or in a pathogen-infected cell;

- b. searching one or more data structures to obtain one or more sets of information, wherein the one or more sets of information comprises one or more expressed enzymes associated with one or more respective classes of organisms that is different than the target organism; and
  - c. comparing the first set of information to the one or more sets of information to create a first output, wherein the first output comprises target enzymes in the first set of information that are not present in the one or more sets of information, and wherein the target enzymes are drug targets.
19. The method of claim 18, wherein the enzymes are expressed by the target organism or in a pathogen infected cell, but absent in the classes of organism of step b.
  20. The method of claim 18, wherein the target organism is selected from the group consisting of bacteria, parasites, rickettsia, virus, and fungus.
  21. The method of claim 18, wherein the organism of step b is an animal or plant.
  22. The method of claim 18, wherein the animal is a mammal.
  23. The method of claim 18, wherein the comparison step utilizes an alignment search algorithm.
  24. The method of claim 18, wherein the alignment search algorithm is a Needleman-Wunsch global alignment algorithm, a Smith-Waterman local alignment algorithm, a "FAST" algorithm, or a BLAST algorithm.
  25. The method of claim 18, further comprising the step of outputting a list of the target enzymes.

26. The method of claim 18, further comprising the step of comparing the first output to a data structure of metabolic enzymes, wherein the metabolic data structure contains enzymes present in metabolic pathways, to obtain a set of metabolic target enzymes, wherein the  
5 metabolic target enzymes are enzymes present in both the first output and in the metabolic data structure, and a set of non-metabolic target enzymes, wherein the non-metabolic target enzymes are enzymes present in the first output but not in the metabolic data structure.
27. The method of claim 26, further comprising the step of displaying the  
10 metabolic enzymes and the non-metabolic enzymes in a manner such that the metabolic enzymes are distinguishable from the non-metabolic enzymes.
28. The method of claim 18, wherein the searching steps utilize a network.
29. The method of claim 18, wherein the network is capable of searching  
15 the one or more data structures, wherein the one or more data structures are stored on a plurality of servers connected to the network.
30. The method of claim 18, wherein the comparing step utilizes a user's computer.
31. The method of claim 18, wherein the first set of information comprises  
20 information about Enzyme Commission numbers relating to the first set of enzymes associated with the target organism.
32. The method of claim 18, wherein the one or more data structures comprise information about Enzyme Commission numbers relating to the one or more expressed enzymes.
33. The method of claim 18, wherein the one or more data structures  
25 comprises a public domain database.

34. The method of claim 18, further comprising the additional step of using target enzymes to design iECTA compounds.

35. A method for identifying drug targets, the method comprising:

- 5           a. searching the first data structure to obtain the first set of information, wherein the first set of information comprises first enzymes associated with a target organism;
- b. searching a second data structure to obtain a second set of information, wherein the second set of information comprises second enzymes associated with a first class of organism;
- 10          c. comparing the first set of information to the second set of information to create the first output, wherein the first output comprises enzymes in the first set of information that are not present in the second set of information, and wherein the identified enzymes are drug targets;
- 15          d. searching a third data structure to obtain a third set of information relating to third expressed enzymes associated with a second class of organism, wherein the second class of organism is different from the first class of organism, wherein the third expressed enzymes are expressed at elevated levels in the second class of organism; and
- 20           e. comparing the first output with the third set of information to create a second output, wherein the second output identifies enzymes in the first output that are not present in the third set of information, and wherein the target enzymes are drug targets.
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36. The method of claim 35, further comprising repeating steps (d)-(e)  $n$  times, wherein there are  $n$  data structures.

37. The method of claim 35, wherein the drug targets are Enzyme Catalyzed Therapeutic Activation (“ECTA”) targets.
38. The method of claim 35, wherein the comparison step utilizes an alignment search algorithm.
- 5 39. The method of claim 38, wherein the alignment search algorithm is a Needleman-Wunsch global alignment algorithm, a Smith-Waterman local alignment algorithm, a “FAST” algorithm, or a BLAST algorithm.
- 10 40. The method of claim 35, further comprising the step of outputting a list of the target enzymes.
- 15 41. The method of claim 35, further comprising the step of comparing the target enzymes to a data structure of metabolic enzymes, wherein the metabolic data structure contains enzymes present in metabolic pathways, to obtain a set of metabolic target enzymes, wherein the metabolic target enzymes are both target enzymes and present in the metabolic data structure, and a set of non-metabolic target enzymes, wherein the non-metabolic target enzymes are target enzymes but are not in the metabolic data structure.
- 20 42. The method of claim 41, further comprising the step of displaying the metabolic enzymes and the non-metabolic enzymes in a manner such that the metabolic enzymes are distinguishable from the non-metabolic enzymes.
43. The method of claim 35, wherein the searching steps utilize a network.
- 25 44. The method of claim 35, wherein the network is capable of searching the  $n$  data structures, wherein the  $n$  data structures are stored on a one or more servers connected to the network.

45. The method of claim 35, wherein the comparing steps utilize a user's computer.
46. The method of claim 35, wherein the first set of information comprises information about Enzyme Commission numbers relating to the first enzymes associated with the target organism.
47. The method of claim 35, wherein any of the  $n$  data structures in the group comprises information about Enzyme Commission numbers.
48. The method of claim 35, wherein any of the  $n$  data structures comprise a public domain database.
49. The method of claim 35, wherein the class of organism is an animal or a plant.
50. The method of claim 49, wherein the animal is a mammal.
51. The method of claim 35, further comprising the step of using the target enzymes to design ECTA compounds.
52. A system for identifying enzymes for designing Enzyme Catalyzed Therapeutic Activation (ECTA) compounds, comprising:
- a. searching a first data structure to obtain a first set of information, wherein the first set of information comprises first enzymes associated with a target organism;
  - b. searching one or more data structures to obtain one or more sets of information, wherein the one or more sets of information comprises one or logic for searching a first data structure to obtain a first set of information relating to one or more enzymes associated with a target organism;
  - c. logic for searching one or more other data structures to obtain one or more additional sets of information relating to one or

more expressed enzymes associated with one or more additional classes of organisms; and

- 5           d. logic for comparing the first set of information to the one or more additional sets of information to identify enzymes in the first set of information that are not present in the one or more additional sets of information, wherein the identified enzymes are capable of being used to design ECTA compounds.
53. The system of claim 52, further comprising logic for outputting a list of the identified enzymes.
- 10       54. The system of claim 52, further comprising: logic for organizing the identified enzymes into a first set of enzymes capable of being placed into metabolic pathways and a second set of enzymes not capable of being placed into metabolic pathways; and logic for displaying the first and second sets of enzymes such that the first set of enzymes are distinguishable from the second set of enzymes.
- 15       55. The system of claim 52, wherein a third data structure is queried to organize the identified enzymes.
56. The system of claim 52, wherein a network is utilized to search at least one of the first data structure and the second data structure.
- 20       57. The system of claim 56, wherein the network is capable of communicating utilizing TCP/IP or IPX protocols.
58. The system of claim 52, wherein the information relating to the one or more enzymes of the target organism includes information about Enzyme Commission (EC) numbers of the one or more enzymes.
- 25       59. The system of claim 52, wherein the one or more additional sets of information relating to the one or more expressed enzymes associated with one or more classes of organisms includes information about

Enzyme Commission (EC) numbers of the one or more expressed enzymes.

5 60. A computer program product for identifying enzymes for designing Enzyme Catalyzed Therapeutic Activation (ECTA) compounds, comprising:

- 10 a. computer code for searching a first data structure to obtain a first set of information relating to one or more enzymes associated with a target organism;
- b. computer code for searching one or more other data structures to obtain one or more additional sets of information relating to one or more expressed enzymes associated with one or more additional classes of organisms; and
- 15 c. computer code for comparing the first set of information to the one or more additional sets of information to identify enzymes in the first set of information that are not present in the one or more additional sets of information, wherein the identified enzymes are capable of being used to design ECTA compounds.

20 61. The computer program product of claim 60, further comprising computer code for outputting a list of the identified enzymes.

25 62. The computer program product of claim 60, further comprising: computer code for organizing the identified enzymes into a first set of enzymes capable of being placed into metabolic pathways and a second set of enzymes not capable of being placed into metabolic pathways; and computer code for displaying the first and second sets of enzymes such that the first set of enzymes are distinguishable from the second set of enzymes.

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69. The method of claim 68, wherein the iECTA enzyme is selected from the group of enzymes listed in Figures 7A and B and their biological equivalents.

70. The method of claim 69, wherein the iECTA enzymes beta-lactamase and peptide deformylase are specifically excluded.

71. The method of claim 69, wherein the iECTA enzyme is a member of an enzyme selected from the group consisting of the enzymes designated EC1, EC2, EC3, EC4, EC5, and EC6.
72. The method of claim 69, wherein the organism is selected from the group consisting of bacteria, parasites, rickettsia, virus, and fungus.
73. The method of claim 69, wherein the host is an animal or plant.
74. The method of claim 73, wherein the animal is a mammal.
75. A method for treating an infection caused by a pathogen expressing an iECTA enzyme or a host cell expressing an iECTA enzyme in a subject, comprising administering to the subject an effective amount of an iECTA prodrug that is activated to a toxin in the pathogen or cell by the iECTA enzyme, thereby alleviating the symptoms.
76. The method of claim 75, wherein the iECTA enzyme is selected from the group of enzymes listed in Figures 7A and B and their biological equivalents.
77. The method of claim 75, wherein the iECTA enzymes beta-lactamase and peptide deformylase are specifically excluded.
78. The method of claim 75, wherein the iECTA enzyme is a member of an enzyme selected from the group consisting of the enzymes designated EC1, EC2, EC3, EC4, EC5, and EC6.
79. The method of claim 75, wherein the organism is selected from the group consisting of bacteria, parasites, rickettsia, virus, and fungus.
80. The method of claim 75, wherein the host is an animal or plant.
81. The method of claim 80, wherein the animal is a mammal.